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WHAT IS CLAIMED IS:

- 1. A method for identifying a peptide-peptide interaction comprising:
 - (a) providing a first fusion construct comprising target peptide fused to a first DNA binding domain;
 - (b) providing a second fusion construct comprising a library encoded peptide (LEP) fused to second DNA binding domain (DBD), wherein said second DBD works as a complex with said first DBD to facilitate binding of said complex to a prokaryotic operator region;
- (c) contacting said first and second fusion constructs in a prokaryotic host cell which comprises said prokaryotic operator region, wherein said prokaryotic operator region is operationally linked to a coding region for one or more indicator polypeptides; and
 - (d) determining binding of said complex to said operator region,
- whereby binding of said complex to said operator region identifies said LEP as a binding partner for said target peptide.
 - 2. The method of claim 1, wherein binding of said complex to said operator acts blocks the transcription of said coding region.
- 3. The method of claim 1, wherein said one or more indicator polypeptides render said prokaryotic host cell insensitive to phage infection.
 - 4. The method of claim 3, wherein step (d) comprises infection with a phage that infects, replicates and lyses said prokaryotic host cell.
 - 5. The method of claim 4, wherein said operator is the lacZ operator, and the first and second DBDs are derived from the λ repressor.

- 6. The method of claim 1, wherein one or more indicator polypeptides produce a colorimetric or fluorescent product.
- 7. The method of claim 1, wherein said one or more indicator polypeptides is β -gal.
- 8. The method of claim 1, wherein said target peptide is 5 to about 5000 residues in length.
 - 9. The method of claim 1, wherein said target peptide is 10 to about 2000 residues in length.
 - 10. The method of claim 1, wherein said LEP is 5 to about 50 residues.
- 11. The method of claim 1, wherein said first and second fusion constructs are encoded by a nucleic acid segment under the control of a promoter operable in said prokaryotic host cell.
 - 12. The method of claim 1, wherein said target peptide and LEP bind with an affinity in the range of about 10^{-3} to about 10^{-6} M.
 - 13. The method of claim 12, wherein said target peptide and LEP bind with an affinity in the range of about 10⁻⁴ M.
 - 14. The method of claim 12, wherein said target peptide and LEP bind with an affinity in the range of about 10⁻⁵ M.
 - 15. The method of claim 12, wherein said target peptide and LEP bind with an affinity in the range of about 10⁻⁶ M.
- 20 16. The method of claim 1, further comprising random mutagenesis of said LEP, followed by measuring the change, if any, in the binding affinity of said LEP for said target.
 - 17. The method of claim 16, wherein said measuring comprises effecting binding of said LEP to said target peptide under conditions more stringent than in claim 1.

- 18. The method of claim 1, further comprising:
 - (e) linking said identified LEP to a third peptide, whereby said linking permits said identified LEP and said third peptide to interact independently with said target peptide;
- 5 (f) then contacting said target peptide with the identified LEP-third peptide complex, and
 - (g) followed by determining the change, if any, in the binding affinity of said LEP for said target peptide.
- 19. The method of claim 18, wherein said measuring comprises effecting binding of said LEP to said target peptide under conditions more stringent than in claim 1.
 - 20. The method of claim 18, wherein said third peptide is known to bind said target peptide.
 - 21. The method of claim 18, wherein said third peptide is a member of a peptide or peptidomimetic library.
- The method of claim 1, wherein said target peptide is an enzyme substrate, an antigen, or a eukaryotic cell antigen.
 - 23. The method of claim 22, wherein said target peptide is an enzyme substrate.
 - 24. The method of claim 23, wherein said enzyme substrate is bacterial, viral or fungal antigen.
- 25. The method of claim 22, wherein said target peptide is a eukaryotic cell antigen.
 - 26. The method of claim 25, wherein said eukaryotic cell antigen is a tumor cell marker, an HLA antigen, a cell surface receptor, or a cell surface transporter.
 - 27. The method of claim 1, further comprising, prior to said determining, the step of stabilizing the interaction between said target peptide and said LEP.

- 28. The method of claim 27, wherein said stabilizing is achieved via cross-linking or phototrapping.
- 29. The method of claim 1, wherein said first peptide comprises a multimer of a smaller peptide unit.
- 5 30. The method of claim 1, further comprising assessing binding of said target peptide to said identified LEP by Western blot, mass spectroscopy, or nuclear magnetic resonance.
 - 31. A method for screening a peptide library for peptide-peptide interactions comprising:
- 10 (a) providing a plurality of a first fusion construct comprising a target peptide fused to a first DNA binding domain;
 - (b) providing a plurality of second fusion construct comprising a library of encoded peptide (LEPs) fused to second DNA binding domain (DBD), wherein said second DBD works as a complex with said first DBD to facilitate binding of said complex to a prokaryotic operator region;
 - (c) transferring said pluralities of first and second fusion constructs into a prokaryotic host cell which comprises said prokaryotic operator region, wherein said prokaryotic operator region is operationally linked to a coding region for one or more indicator polypeptides; and
- (d) determining binding of complexes to said operator region,whereby binding of said complexes to said operator region identifies associatedLEPs as binding partners for said target peptide.
 - 32. The method of claim 3, wherein steps (a)-(d) are repeated at least once using the LEP identified in step (d).

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- 33. The method of claim 31, wherein said LEPs are synthesized from a four base cutter-digested DNA library.
- 34. The method of claim 33, further comprising the step of sequencing a DNA encoding an identified LEP.
- 5 35. A library encoded peptide (LEP) selected according to a method comprising:
 - (a) providing a first fusion construct comprising target peptide fused to a first DNA binding domain;
 - (b) providing a second fusion construct comprising said LEP fused to second DNA binding domain (DBD), wherein said second DBD works as a complex with said first DBD to facilitate binding of said complex to a prokaryotic operator region;
 - (c) contacting said first and second fusion constructs in a prokaryotic host cell comprising said prokaryotic operator region, wherein said prokaryotic operator regions is operationally linked to a coding region for one or more indicator polypeptides; and
 - (d) determining binding of said complex to said operator region,
 whereby binding of said complex to said operator region identifies said
 LEP as a binding partner for said target peptide.
 - 36. A heterodimeric binding molecule comprising:
 - (a) a first peptide that binds to a target molecule;
 - (b) a second peptide that binds to said target molecule,

wherein at least one of said first and second peptides is a member of a peptide library; and

- (c) a linker molecule connecting said first and second peptides such that the linking permits said first and second peptides to interact independently with said target molecule.
- 37. The binding molecule of claim 36, further comprising a moiety that permits recovery of said molecule.
- 38. The binding molecule of claim 37, wherein said moiety is a magnetic bead.
- 39. The binding molecule of claim 36, wherein said heterodimeric binding molecule is expressed on the surface of a phage.